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	10	20	30	40	50	60	
1	HHNGTNGTMMQYFEWYLPNDGNHWNRLRDDAANLKS					GITAVWIPPAWK	60
3	-AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLG					ITALWLPPAYK	59
2	HHNGTNGTMMQYFEWHLPNDDGNHWNRLRDDASNLRN					GITAIWIPPAWK	60
4	HHNGTNGTMMQYFEWYLPNDGNHWNRLNSDASNLSK					GITAVWIPPAWK	60
	70	80	90	100	110	120	
1	YDLYDLGEFNQKGTVRTKYGTRNQLQAAVTS					LKNNGIQVYGDV	120
3	YDLYDLGEFNQKGTVRTKYGTRKQYQLQAIQAAHA					AGMQVYADV	119
2	YDLYDLGEFNQKGTVRTKYGTRSQLESIAIHALKNN					GVQVYGDV	120
4	YDLYDLGEFNQKGTVRTKYGTRSQLQAAVTS					LKNNGIQVYGDV	120
	130	140	150	160	170	180	
1	EVNRSNRNQETSGEYAI					EAWTKFDFPGRG	180
3	EVNPSDRNQEISGT					YQIQA	178
2	EVNPNNRNQEISGDY					TEAWTKFDFPGRG	180
4	EVNPNNRNQEVTGEY					TEAWTRFDFPGRG	180
	190	200	210	220	230	240	
1	RGTGKAWDWEVDTE					NGNYDYL	240
3	RGIGKAWDWEVDTE					NGNYDYL	238
2	RGDGKAWDWEVDSE					NGNYDYL	240
4	RGHGKAWDWEVDTE					NGNYDYL	240
	250	260	270	280	290	300	
1	IKYSFTRDWLTHVR					NNTGKPMFA	300
3	IKFSFFPDWLSY					VRSQTGKPL	298
2	IKYSFTRDWLTHVR					NATGKEMFA	300
4	IKYSFTRDWLTHVR					SATGKNMFA	300
	310	320	330	340	350	360	
1	SNSGGYDMRNILNG					SVVQKHP	360
3	SKSGGAFDMRTL					TMTNTLMK	358
2	SNSGGYDMRNILNG					TMTNTLMK	360
4	SKSGGNYDMRNIF					NGTVVQK	360
	370	380	390	400	410	420	
1	QGYP					SVFYGDY	420
3	EGYPCV					FYGDY	418
2	QGYP					SVFYGDY	420
4	QGYP					SVFYGDY	420
	430	440	450	460	470	480	
1	HPNSGLATIMSDG					PGGKWMY	480
3	KPGSGLAALITD					PGGSKWMY	478
2	HPNSGLATIMSDG					PGGKWMY	480
4	HPNSGLATIMSDG					AGGSKWMF	480
	490	500	510	520	530	540	
1	VWVKQ						485
3	VWVPRKTTVSTI					ARPI	514
2	IWKVR						485
4	IWNK						485

Fig. 1

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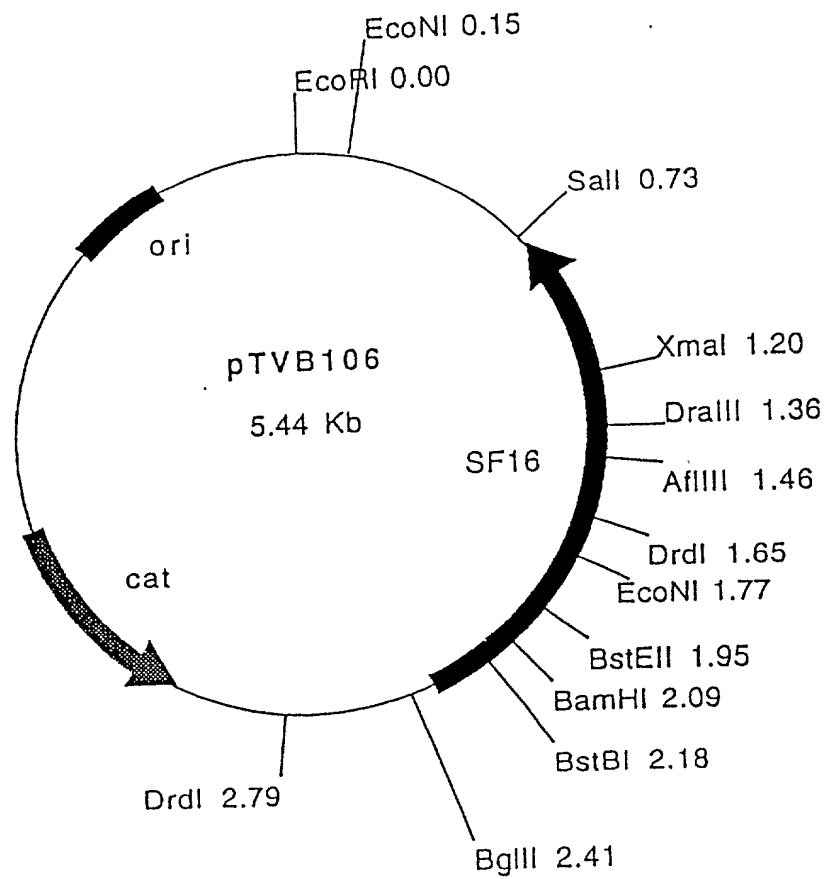


Fig. 2

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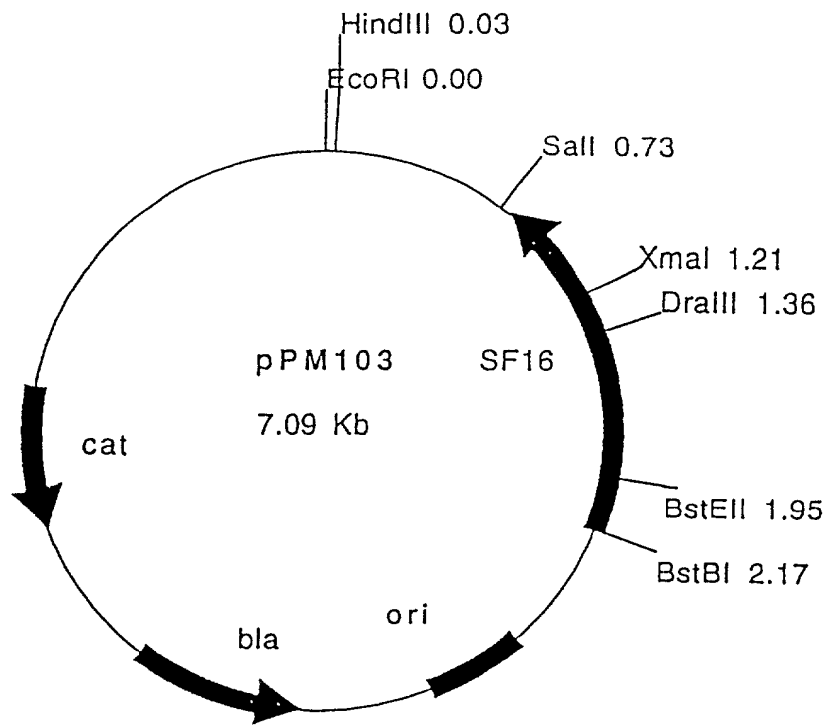


Fig. 3

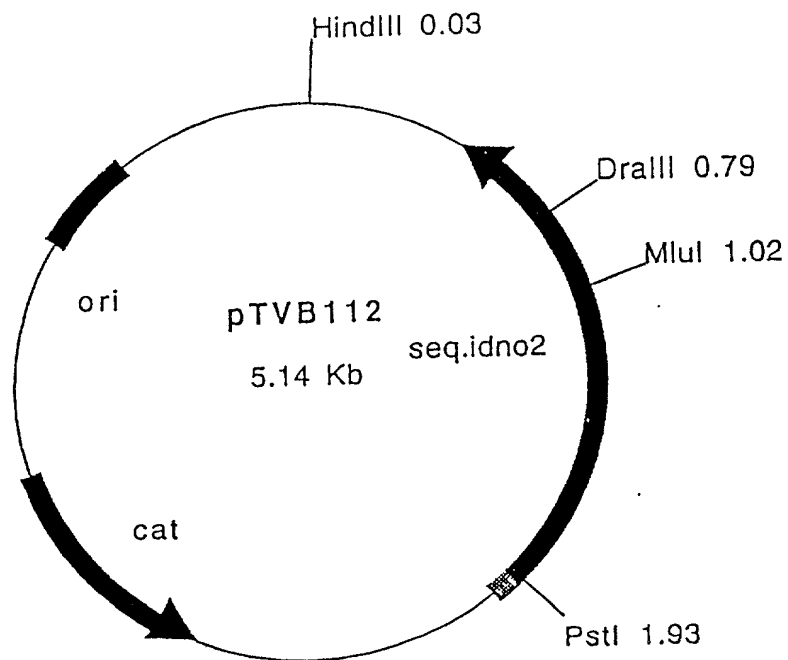


Fig. 4

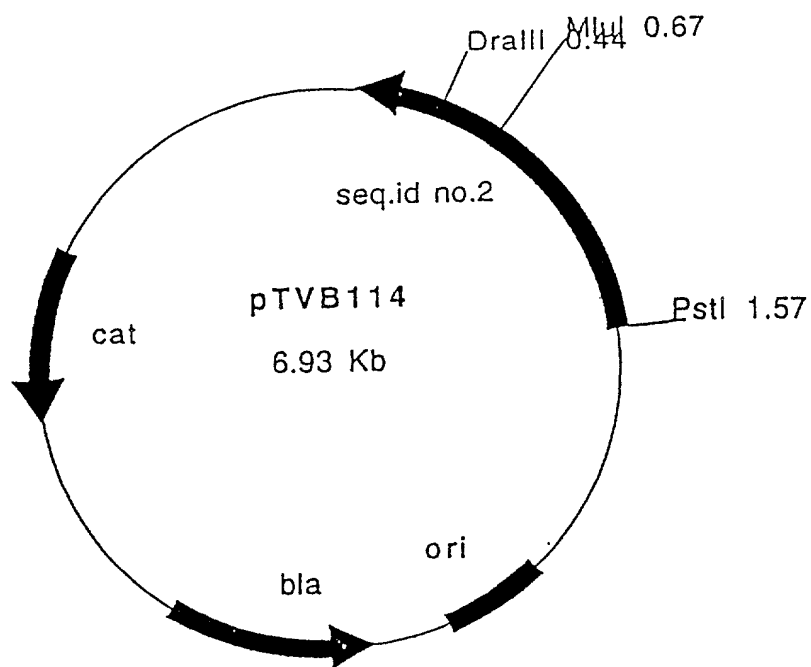


Fig. 5